



1

SEQUENCE LISTING

<110> PAKOLA, STEVE
DE SMET, MARK

<120> PHARMACOLOGICAL VITREOLYSIS

<130> 113476.122

<140> 10/729,475

<141> 2003-12-05

<150> GB 0228409.9

<151> 2002-12-06

<160> 15

<170> PatentIn Ver. 3.2

<210> 1

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 1

ggggtatctc tcgagaaaag agccccttca ttgtattg

38

<210> 2

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 2

gtttttgttc tagattaatt atttctcatc actccctc

38

<210> 3

<211> 750

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(747)

<400> 3

gcc cct tca ttt gat tgt ggg aag cct caa gtg gag ccg aag aaa tgt
Ala Pro Ser Phe Asp Cys Gly Lys Pro Gln Val Glu Pro Lys Lys Cys
1 5 10 15

48

cct gga agg gtt gtg ggg ggg tgt gtg gcc cac cca cat tcc tgg ccc	96
Pro Gly Arg Val Val Gly Gly Cys Val Ala His Pro His Ser Trp Pro	
20 25 30	
tgg caa gtc agt ctt aga aca agg ttt gga atg cac ttc tgt gga ggc	144
Trp Gln Val Ser Leu Arg Thr Arg Phe Gly Met His Phe Cys Gly Gly	
35 40 45	
acc ttg ata tcc cca gag tgg gtg ttg act gct gcc cac tgc ttg gag	192
Thr Leu Ile Ser Pro Glu Trp Val Leu Thr Ala Ala His Cys Leu Glu	
50 55 60	
aag tcc cca agg cct tca tcc tac aag gtc atc ctg ggt gca cac caa	240
Lys Ser Pro Arg Pro Ser Ser Tyr Lys Val Ile Leu Gly Ala His Gln	
65 70 75 80	
gaa gtg aat ctc gaa ccg cat gtt cag gaa ata gaa gtg tct agg ctg	288
Glu Val Asn Leu Glu Pro His Val Gln Glu Ile Glu Val Ser Arg Leu	
85 90 95	
ttc ttg gag ccc aca cga aaa gat att gcc ttg cta aag cta agc agt	336
Phe Leu Glu Pro Thr Arg Lys Asp Ile Ala Leu Leu Lys Leu Ser Ser	
100 105 110	
cct gcc gtc atc act gac aaa gta atc cca gct tgt ctg cca tcc cca	384
Pro Ala Val Ile Thr Asp Lys Val Ile Pro Ala Cys Leu Pro Ser Pro	
115 120 125	
aat tat gtg gtc gct gac cgg acc gaa tgt ttc atc act ggc tgg gga	432
Asn Tyr Val Val Ala Asp Arg Thr Glu Cys Phe Ile Thr Gly Trp Gly	
130 135 140	
gaa acc caa ggt act ttt gga gct ggc ctt ctc aag gaa gcc cag ctc	480
Glu Thr Gln Gly Thr Phe Gly Ala Gly Leu Leu Lys Glu Ala Gln Leu	
145 150 155 160	
cct gtg att gag aat aaa gtg tgc aat cgc tat gag ttt ctg aat gga	528
Pro Val Ile Glu Asn Lys Val Cys Asn Arg Tyr Glu Phe Leu Asn Gly	
165 170 175	
aga gtc caa tcc acc gaa ctc tgt gct ggg cat ttg gcc gga ggc act	576
Arg Val Gln Ser Thr Glu Leu Cys Ala Gly His Leu Ala Gly Gly Thr	
180 185 190	
gac agt tgc cag ggt gac agt gga ggt cct ctg gtt tgc ttc gag aag	624
Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Phe Glu Lys	
195 200 205	
gac aaa tac att tta caa gga gtc act tct tgg ggt ctt ggc tgt gca	672
Asp Lys Tyr Ile Leu Gln Gly Val Thr Ser Trp Gly Leu Gly Cys Ala	
210 215 220	
cgc ccc aat aag cct ggt gtc tat gtt cgt gtt tca agg ttt gtt act	720
Arg Pro Asn Lys Pro Gly Val Tyr Val Arg Val Ser Arg Phe Val Thr	
225 230 235 240	

tgg att gag gga gtg atg aga aat aat taa
 Trp Ile Glu Gly Val Met Arg Asn Asn
 245

750

<210> 4
 <211> 249
 <212> PRT
 <213> Homo sapiens

<400> 4
 Ala Pro Ser Phe Asp Cys Gly Lys Pro Gln Val Glu Pro Lys Lys Cys
 1 5 10 15
 Pro Gly Arg Val Val Gly Gly Cys Val Ala His Pro His Ser Trp Pro
 20 25 30
 Trp Gln Val Ser Leu Arg Thr Arg Phe Gly Met His Phe Cys Gly Gly
 35 40 45
 Thr Leu Ile Ser Pro Glu Trp Val Leu Thr Ala Ala His Cys Leu Glu
 50 55 60
 Lys Ser Pro Arg Pro Ser Ser Tyr Lys Val Ile Leu Gly Ala His Gln
 65 70 75 80
 Glu Val Asn Leu Glu Pro His Val Gln Glu Ile Glu Val Ser Arg Leu
 85 90 95
 Phe Leu Glu Pro Thr Arg Lys Asp Ile Ala Leu Leu Lys Leu Ser Ser
 100 105 110
 Pro Ala Val Ile Thr Asp Lys Val Ile Pro Ala Cys Leu Pro Ser Pro
 115 120 125
 Asn Tyr Val Val Ala Asp Arg Thr Glu Cys Phe Ile Thr Gly Trp Gly
 130 135 140
 Glu Thr Gln Gly Thr Phe Gly Ala Gly Leu Leu Lys Glu Ala Gln Leu
 145 150 155 160
 Pro Val Ile Glu Asn Lys Val Cys Asn Arg Tyr Glu Phe Leu Asn Gly
 165 170 175
 Arg Val Gln Ser Thr Glu Leu Cys Ala Gly His Leu Ala Gly Gly Thr
 180 185 190
 Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Phe Glu Lys
 195 200 205
 Asp Lys Tyr Ile Leu Gln Gly Val Thr Ser Trp Gly Leu Gly Cys Ala
 210 215 220
 Arg Pro Asn Lys Pro Gly Val Tyr Val Arg Val Ser Arg Phe Val Thr
 225 230 235 240
 Trp Ile Glu Gly Val Met Arg Asn Asn
 245

<210> 5
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 Primer

<400> 5
 ggggtatctc tcgagaaaag agcacctccg cctgttggtcc tgcttcc 47

<210> 6
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 Primer

<400> 6
 gcagtgggct gcagtcaaca cccactc 27

<210> 7
 <211> 1047
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1044)

<400> 7
 gca cct ccg cct gtt gtc ctg ctt cca gat gta gag act cct tcc gaa 48
 Ala Pro Pro Pro Val Val Leu Leu Pro Asp Val Glu Thr Pro Ser Glu
 1 5 10 15

gaa gac tgt atg ttt ggg aat ggg aaa gga tac cga ggc aag agg gcg 96
 Glu Asp Cys Met Phe Gly Asn Gly Lys Gly Tyr Arg Gly Lys Arg Ala
 20 25 30

acc act gtt act ggg acg cca tgc cag gac tgg gct gcc cag gag ccc 144
 Thr Thr Val Thr Gly Thr Pro Cys Gln Asp Trp Ala Ala Gln Glu Pro
 35 40 45

cat aga cac agc att ttc act cca gag aca aat cca cgg gcg ggt ctg 192
 His Arg His Ser Ile Phe Thr Pro Glu Thr Asn Pro Arg Ala Gly Leu
 50 55 60

gaa aaa aat tac tgc cgt aac cct gat ggt gat gta ggt ggt ccc tgg 240
 Glu Lys Asn Tyr Cys Arg Asn Pro Asp Gly Asp Val Gly Gly Pro Trp
 65 70 75 80

tgc tac acg aca aat cca aga aaa ctt tac gac tac tgt gat gtc cct	288
Cys Tyr Thr Thr Asn Pro Arg Lys Leu Tyr Asp Tyr Cys Asp Val Pro	
85 90 95	
cag tgt gcg gcc cct tca ttt gat tgt ggg aag cct caa gtg gag ccg	336
Gln Cys Ala Ala Pro Ser Phe Asp Cys Gly Lys Pro Gln Val Glu Pro	
100 105 110	
aag aaa tgt cct gga agg gtt gtg ggg ggg tgt gtg gcc cac cca cat	384
Lys Lys Cys Pro Gly Arg Val Val Gly Gly Cys Val Ala His Pro His	
115 120 125	
tcc tgg ccc tgg caa gtc agt ctt aga aca agg ttt gga atg cac ttc	432
Ser Trp Pro Trp Gln Val Ser Leu Arg Thr Arg Phe Gly Met His Phe	
130 135 140	
tgt gga ggc acc ttg ata tcc cca gag tgg gtg ttg act gct gcc cac	480
Cys Gly Gly Thr Leu Ile Ser Pro Glu Trp Val Leu Thr Ala Ala His	
145 150 155 160	
tgc ttg gag aag tcc cca agg cct tca tcc tac aag gtc atc ctg ggt	528
Cys Leu Glu Lys Ser Pro Arg Pro Ser Ser Tyr Lys Val Ile Leu Gly	
165 170 175	
gca cac caa gaa gtg aat ctc gaa ccg cat gtt cag gaa ata gaa gtg	576
Ala His Gln Glu Val Asn Leu Glu Pro His Val Gln Glu Ile Glu Val	
180 185 190	
tct agg ctg ttc ttg gag ccc aca cga aaa gat att gcc ttg cta aag	624
Ser Arg Leu Phe Leu Glu Pro Thr Arg Lys Asp Ile Ala Leu Leu Lys	
195 200 205	
cta agc agt cct gcc gtc atc act gac aaa gta atc cca gct tgt ctg	672
Leu Ser Ser Pro Ala Val Ile Thr Asp Lys Val Ile Pro Ala Cys Leu	
210 215 220	
cca tcc cca aat tat gtg gtc gct gac cgg acc gaa tgt ttc atc act	720
Pro Ser Pro Asn Tyr Val Val Ala Asp Arg Thr Glu Cys Phe Ile Thr	
225 230 235 240	
ggc tgg gga gaa acc caa ggt act ttt gga gct ggc ctt ctc aag gaa	768
Gly Trp Gly Glu Thr Gln Gly Thr Phe Gly Ala Gly Leu Leu Lys Glu	
245 250 255	
gcc cag ctc cct gtg att gag aat aaa gtg tgc aat cgc tat gag ttt	816
Ala Gln Leu Pro Val Ile Glu Asn Lys Val Cys Asn Arg Tyr Glu Phe	
260 265 270	
ctg aat gga aga gtc caa tcc acc gaa ctc tgt gct ggg cat ttg gcc	864
Leu Asn Gly Arg Val Gln Ser Thr Glu Leu Cys Ala Gly His Leu Ala	
275 280 285	
gga ggc act gac agt tgc cag ggt gac agt gga ggt cct ctg gtt tgc	912
Gly Gly Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys	
290 295 300	

ttc gag aag gac aaa tac att tta caa gga gtc act tct tgg ggt ctt 960
 Phe Glu Lys Asp Lys Tyr Ile Leu Gln Gly Val Thr Ser Trp Gly Leu
 305 310 315 320
 ggc tgt gca cgc ccc aat aag cct ggt gtc tat gtt cgt gtt tca agg 1008
 Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Val Arg Val Ser Arg
 325 330 335
 ttt gtt act tgg att gag gga gtg atg aga aat aat taa 1047
 Phe Val Thr Trp Ile Glu Gly Val Met Arg Asn Asn
 340 345

<210> 8
 <211> 348
 <212> PRT
 <213> Homo sapiens

<400> 8
 Ala Pro Pro Pro Val Val Leu Leu Pro Asp Val Glu Thr Pro Ser Glu
 1 5 10 15
 Glu Asp Cys Met Phe Gly Asn Gly Lys Gly Tyr Arg Gly Lys Arg Ala
 20 25 30
 Thr Thr Val Thr Gly Thr Pro Cys Gln Asp Trp Ala Ala Gln Glu Pro
 35 40 45
 His Arg His Ser Ile Phe Thr Pro Glu Thr Asn Pro Arg Ala Gly Leu
 50 55 60
 Glu Lys Asn Tyr Cys Arg Asn Pro Asp Gly Asp Val Gly Gly Pro Trp
 65 70 75 80
 Cys Tyr Thr Thr Asn Pro Arg Lys Leu Tyr Asp Tyr Cys Asp Val Pro
 85 90 95
 Gln Cys Ala Ala Pro Ser Phe Asp Cys Gly Lys Pro Gln Val Glu Pro
 100 105 110
 Lys Lys Cys Pro Gly Arg Val Val Gly Gly Cys Val Ala His Pro His
 115 120 125
 Ser Trp Pro Trp Gln Val Ser Leu Arg Thr Arg Phe Gly Met His Phe
 130 135 140
 Cys Gly Gly Thr Leu Ile Ser Pro Glu Trp Val Leu Thr Ala Ala His
 145 150 155 160
 Cys Leu Glu Lys Ser Pro Arg Pro Ser Ser Tyr Lys Val Ile Leu Gly
 165 170 175
 Ala His Gln Glu Val Asn Leu Glu Pro His Val Gln Glu Ile Glu Val
 180 185 190
 Ser Arg Leu Phe Leu Glu Pro Thr Arg Lys Asp Ile Ala Leu Leu Lys
 195 200 205

Leu Ser Ser Pro Ala Val Ile Thr Asp Lys Val Ile Pro Ala Cys Leu
 210 215 220
 Pro Ser Pro Asn Tyr Val Val Ala Asp Arg Thr Glu Cys Phe Ile Thr
 225 230 235 240
 Gly Trp Gly Glu Thr Gln Gly Thr Phe Gly Ala Gly Leu Leu Lys Glu
 245 250 255
 Ala Gln Leu Pro Val Ile Glu Asn Lys Val Cys Asn Arg Tyr Glu Phe
 260 265 270
 Leu Asn Gly Arg Val Gln Ser Thr Glu Leu Cys Ala Gly His Leu Ala
 275 280 285
 Gly Gly Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
 290 295 300
 Phe Glu Lys Asp Lys Tyr Ile Leu Gln Gly Val Thr Ser Trp Gly Leu
 305 310 315 320
 Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Val Arg Val Ser Arg
 325 330 335
 Phe Val Thr Trp Ile Glu Gly Val Met Arg Asn Asn
 340 345

<210> 9
 <211> 2376
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(2373)

<400> 9
 gag cct ctg gat gac tat gtg aat acc cag ggg gct tca ctg ttc agt 48
 Glu Pro Leu Asp Asp Tyr Val Asn Thr Gln Gly Ala Ser Leu Phe Ser
 1 5 10 15
 gtc act aag aag cag ctg gga gca gga agt ata gaa gaa tgt gca gca 96
 Val Thr Lys Lys Gln Leu Gly Ala Gly Ser Ile Glu Glu Cys Ala Ala
 20 25 30
 aaa tgt gag gag gac gaa gaa ttc acc tgc agg gca ttc caa tat cac 144
 Lys Cys Glu Glu Asp Glu Glu Phe Thr Cys Arg Ala Phe Gln Tyr His
 35 40 45
 agt aaa gag caa caa tgt gtg ata atg gct gaa aac agg aag tcc tcc 192
 Ser Lys Glu Gln Gln Cys Val Ile Met Ala Glu Asn Arg Lys Ser Ser
 50 55 60
 ata atc att agg atg aga gat gta gtt tta ttt gaa aag aaa gtg tat 240
 Ile Ile Ile Arg Met Arg Asp Val Val Leu Phe Glu Lys Lys Val Tyr
 65 70 75 80

ctc	tca	gag	tgc	aag	act	ggg	aat	gga	aag	aac	tac	aga	ggg	acg	atg	288
Leu	Ser	Glu	Cys	Lys	Thr	Gly	Asn	Gly	Lys	Asn	Tyr	Arg	Gly	Thr	Met	
				85					90					95		
tcc	aaa	aca	aaa	aat	ggc	atc	acc	tgt	caa	aaa	tgg	agt	tcc	act	tct	336
Ser	Lys	Thr	Lys	Asn	Gly	Ile	Thr	Cys	Gln	Lys	Trp	Ser	Ser	Thr	Ser	
			100					105					110			
ccc	cac	aga	cct	aga	ttc	tca	cct	gct	aca	cac	ccc	tca	gag	gga	ctg	384
Pro	His	Arg	Pro	Arg	Phe	Ser	Pro	Ala	Thr	His	Pro	Ser	Glu	Gly	Leu	
			115				120					125				
gag	gag	aac	tac	tgc	agg	aat	cca	gac	aac	gat	ccg	cag	ggg	ccc	tgg	432
Glu	Glu	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Asn	Asp	Pro	Gln	Gly	Pro	Trp	
	130					135					140					
tgc	tat	act	act	gat	cca	gaa	aag	aga	tat	gac	tac	tgc	gac	att	ctt	480
Cys	Tyr	Thr	Thr	Asp	Pro	Glu	Lys	Arg	Tyr	Asp	Tyr	Cys	Asp	Ile	Leu	
145					150					155					160	
gag	tgt	gaa	gag	gaa	tgt	atg	cat	tgc	agt	gga	gaa	aac	tat	gac	ggc	528
Glu	Cys	Glu	Glu	Glu	Cys	Met	His	Cys	Ser	Gly	Glu	Asn	Tyr	Asp	Gly	
				165					170					175		
aaa	att	tcc	aag	acc	atg	tct	gga	ctg	gaa	tgc	cag	gcc	tgg	gac	tct	576
Lys	Ile	Ser	Lys	Thr	Met	Ser	Gly	Leu	Glu	Cys	Gln	Ala	Trp	Asp	Ser	
			180					185					190			
cag	agc	cca	cac	gct	cat	gga	tac	att	cct	tcc	aaa	ttt	cca	aac	aag	624
Gln	Ser	Pro	His	Ala	His	Gly	Tyr	Ile	Pro	Ser	Lys	Phe	Pro	Asn	Lys	
		195					200					205				
aac	ctg	aag	aag	aat	tac	tgt	cgt	aac	ccc	gat	agg	gag	ctg	cgg	cct	672
Asn	Leu	Lys	Lys	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Arg	Glu	Leu	Arg	Pro	
	210			215						220						
tgg	tgt	ttc	acc	acc	gac	ccc	aac	aag	cgc	tgg	gaa	ctt	tgc	gac	atc	720
Trp	Cys	Phe	Thr	Thr	Asp	Pro	Asn	Lys	Arg	Trp	Glu	Leu	Cys	Asp	Ile	
225					230					235					240	
ccc	cgc	tgc	aca	aca	cct	cca	cca	tct	tct	ggt	ccc	acc	tac	cag	tgt	768
Pro	Arg	Cys	Thr	Thr	Pro	Pro	Pro	Ser	Ser	Gly	Pro	Thr	Tyr	Gln	Cys	
				245					250					255		
ctg	aag	gga	aca	ggt	gaa	aac	tat	cgc	ggg	aat	gtg	gct	ggt	acc	ggt	816
Leu	Lys	Gly	Thr	Gly	Glu	Asn	Tyr	Arg	Gly	Asn	Val	Ala	Val	Thr	Val	
			260					265					270			
tcc	ggg	cac	acc	tgt	cag	cac	tgg	agt	gca	cag	acc	cct	cac	aca	cat	864
Ser	Gly	His	Thr	Cys	Gln	His	Trp	Ser	Ala	Gln	Thr	Pro	His	Thr	His	
		275					280					285				
aac	agg	aca	cca	gaa	aac	ttc	ccc	tgc	aaa	aat	ttg	gat	gaa	aac	tac	912
Asn	Arg	Thr	Pro	Glu	Asn	Phe	Pro	Cys	Lys	Asn	Leu	Asp	Glu	Asn	Tyr	
	290					295					300					

tgc cgc aat cct gac gga aaa agg gcc cca tgg tgc cat aca acc aac	960
Cys Arg Asn Pro Asp Gly Lys Arg Ala Pro Trp Cys His Thr Thr Asn	
305 310 315 320	
agc caa gtg cgg tgg gag tac tgt aag ata ccg tcc tgt gac tcc tcc	1008
Ser Gln Val Arg Trp Glu Tyr Cys Lys Ile Pro Ser Cys Asp Ser Ser	
325 330 335	
cca gta tcc acg gaa caa ttg gct ccc aca gca cca cct gag cta acc	1056
Pro Val Ser Thr Glu Gln Leu Ala Pro Thr Ala Pro Pro Glu Leu Thr	
340 345 350	
cct gtg gtc cag gac tgc tac cat ggt gat gga cag agc tac cga ggc	1104
Pro Val Val Gln Asp Cys Tyr His Gly Asp Gly Gln Ser Tyr Arg Gly	
355 360 365	
aca tcc tcc acc acc acc aca gga aag aag tgt cag tct tgg tca tct	1152
Thr Ser Ser Thr Thr Thr Thr Gly Lys Lys Cys Gln Ser Trp Ser Ser	
370 375 380	
atg aca cca cac cgg cac cag aag acc cca gaa aac tac cca aat gct	1200
Met Thr Pro His Arg His Gln Lys Thr Pro Glu Asn Tyr Pro Asn Ala	
385 390 395 400	
ggc ctg aca atg aac tac tgc agg aat cca gat gcc gat aaa ggc ccc	1248
Gly Leu Thr Met Asn Tyr Cys Arg Asn Pro Asp Ala Asp Lys Gly Pro	
405 410 415	
tgg tgt ttt acc aca gac ccc agc gtc agg tgg gag tac tgc aac ctg	1296
Trp Cys Phe Thr Thr Asp Pro Ser Val Arg Trp Glu Tyr Cys Asn Leu	
420 425 430	
aaa aaa tgc tca gga aca gaa gcg agt gtt gta gca cct ccg cct gtt	1344
Lys Lys Cys Ser Gly Thr Glu Ala Ser Val Val Ala Pro Pro Pro Val	
435 440 445	
gtc ctg ctt cca gat gta gag act cct tcc gaa gaa gac tgt atg ttt	1392
Val Leu Leu Pro Asp Val Glu Thr Pro Ser Glu Glu Asp Cys Met Phe	
450 455 460	
ggg aat ggg aaa gga tac cga ggc aag agg gcg acc act gtt act ggg	1440
Gly Asn Gly Lys Gly Tyr Arg Gly Lys Arg Ala Thr Thr Val Thr Gly	
465 470 475 480	
acg cca tgc cag gac tgg gct gcc cag gag ccc cat aga cac agc att	1488
Thr Pro Cys Gln Asp Trp Ala Ala Gln Glu Pro His Arg His Ser Ile	
485 490 495	
ttc act cca gag aca aat cca cgg gcg ggt ctg gaa aaa aat tac tgc	1536
Phe Thr Pro Glu Thr Asn Pro Arg Ala Gly Leu Glu Lys Asn Tyr Cys	
500 505 510	
cgt aac cct gat ggt gat gta ggt ggt ccc tgg tgc tac acg aca aat	1584
Arg Asn Pro Asp Gly Asp Val Gly Gly Pro Trp Cys Tyr Thr Thr Asn	
515 520 525	

cca aga aaa ctt tac gac tac tgt gat gtc cct cag tgt gcg gcc cct	1632
Pro Arg Lys Leu Tyr Asp Tyr Cys Asp Val Pro Gln Cys Ala Ala Pro	
530 535 540	
tca ttt gat tgt ggg aag cct caa gtg gag ccg aag aaa tgt cct gga	1680
Ser Phe Asp Cys Gly Lys Pro Gln Val Glu Pro Lys Lys Cys Pro Gly	
545 550 555 560	
agg gtt gtg ggg ggg tgt gtg gcc cac cca cat tcc tgg ccc tgg caa	1728
Arg Val Val Gly Gly Cys Val Ala His Pro His Ser Trp Pro Trp Gln	
565 570 575	
gtc agt ctt aga aca agg ttt gga atg cac ttc tgt gga ggc acc ttg	1776
Val Ser Leu Arg Thr Arg Phe Gly Met His Phe Cys Gly Gly Thr Leu	
580 585 590	
ata tcc cca gag tgg gtg ttg act gct gcc cac tgc ttg gag aag tcc	1824
Ile Ser Pro Glu Trp Val Leu Thr Ala Ala His Cys Leu Glu Lys Ser	
595 600 605	
cca agg cct tca tcc tac aag gtc atc ctg ggt gca cac caa gaa gtg	1872
Pro Arg Pro Ser Ser Tyr Lys Val Ile Leu Gly Ala His Gln Glu Val	
610 615 620	
aat ctc gaa ccg cat gtt cag gaa ata gaa gtg tct agg ctg ttc ttg	1920
Asn Leu Glu Pro His Val Gln Glu Ile Glu Val Ser Arg Leu Phe Leu	
625 630 635 640	
gag ccc aca cga aaa gat att gcc ttg cta aag cta agc agt cct gcc	1968
Glu Pro Thr Arg Lys Asp Ile Ala Leu Leu Lys Leu Ser Ser Pro Ala	
645 650 655	
gtc atc act gac aaa gta atc cca gct tgt ctg cca tcc cca aat tat	2016
Val Ile Thr Asp Lys Val Ile Pro Ala Cys Leu Pro Ser Pro Asn Tyr	
660 665 670	
gtg gtc gct gac cgg acc gaa tgt ttc atc act ggc tgg gga gaa acc	2064
Val Val Ala Asp Arg Thr Glu Cys Phe Ile Thr Gly Trp Gly Glu Thr	
675 680 685	
caa ggt act ttt gga gct ggc ctt ctc aag gaa gcc cag ctc cct gtg	2112
Gln Gly Thr Phe Gly Ala Gly Leu Leu Lys Glu Ala Gln Leu Pro Val	
690 695 700	
att gag aat aaa gtg tgc aat cgc tat gag ttt ctg aat gga aga gtc	2160
Ile Glu Asn Lys Val Cys Asn Arg Tyr Glu Phe Leu Asn Gly Arg Val	
705 710 715 720	
caa tcc acc gaa ctc tgt gct ggg cat ttg gcc gga ggc act gac agt	2208
Gln Ser Thr Glu Leu Cys Ala Gly His Leu Ala Gly Gly Thr Asp Ser	
725 730 735	
tgc cag ggt gac agt gga ggt cct ctg gtt tgc ttc gag aag gac aaa	2256
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Phe Glu Lys Asp Lys	
740 745 750	

gag gga gtg atg aga aat aat taa 2376
Glu Gly Val Met Arg Asn Asn
785 790

<400>	10															
Glu	Pro	Leu	Asp	Asp	Tyr	Val	Asn	Thr	Gln	Gly	Ala	Ser	Leu	Phe	Ser	
1				5					10					15		
Val	Thr	Lys	Lys	Gln	Leu	Gly	Ala	Gly	Ser	Ile	Glu	Glu	Cys	Ala	Ala	
			20					25					30			
Lys	Cys	Glu	Glu	Asp	Glu	Glu	Phe	Thr	Cys	Arg	Ala	Phe	Gln	Tyr	His	
		35					40					45				
Ser	Lys	Glu	Gln	Gln	Cys	Val	Ile	Met	Ala	Glu	Asn	Arg	Lys	Ser	Ser	
	50					55					60					
Ile	Ile	Ile	Arg	Met	Arg	Asp	Val	Val	Leu	Phe	Glu	Lys	Lys	Val	Tyr	
65					70					75					80	
Leu	Ser	Glu	Cys	Lys	Thr	Gly	Asn	Gly	Lys	Asn	Tyr	Arg	Gly	Thr	Met	
				85					90					95		
Ser	Lys	Thr	Lys	Asn	Gly	Ile	Thr	Cys	Gln	Lys	Trp	Ser	Ser	Thr	Ser	
			100					105					110			
Pro	His	Arg	Pro	Arg	Phe	Ser	Pro	Ala	Thr	His	Pro	Ser	Glu	Gly	Leu	
		115					120					125				
Glu	Glu	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Asn	Asp	Pro	Gln	Gly	Pro	Trp	
	130					135					140					
Cys	Tyr	Thr	Thr	Asp	Pro	Glu	Lys	Arg	Tyr	Asp	Tyr	Cys	Asp	Ile	Leu	
145					150					155					160	
Glu	Cys	Glu	Glu	Glu	Cys	Met	His	Cys	Ser	Gly	Glu	Asn	Tyr	Asp	Gly	
				165					170					175		
Lys	Ile	Ser	Lys	Thr	Met	Ser	Gly	Leu	Glu	Cys	Gln	Ala	Trp	Asp	Ser	
			180					185					190			
Gln	Ser	Pro	His	Ala	His	Gly	Tyr	Ile	Pro	Ser	Lys	Phe	Pro	Asn	Lys	
		195					200					205				

Asn	Leu	Lys	Lys	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Arg	Glu	Leu	Arg	Pro	210	215	220	
Trp	Cys	Phe	Thr	Thr	Asp	Pro	Asn	Lys	Arg	Trp	Glu	Leu	Cys	Asp	Ile	225	230	235	240
Pro	Arg	Cys	Thr	Thr	Pro	Pro	Pro	Ser	Ser	Gly	Pro	Thr	Tyr	Gln	Cys	245	250	255	
Leu	Lys	Gly	Thr	Gly	Glu	Asn	Tyr	Arg	Gly	Asn	Val	Ala	Val	Thr	Val	260	265	270	
Ser	Gly	His	Thr	Cys	Gln	His	Trp	Ser	Ala	Gln	Thr	Pro	His	Thr	His	275	280	285	
Asn	Arg	Thr	Pro	Glu	Asn	Phe	Pro	Cys	Lys	Asn	Leu	Asp	Glu	Asn	Tyr	290	295	300	
Cys	Arg	Asn	Pro	Asp	Gly	Lys	Arg	Ala	Pro	Trp	Cys	His	Thr	Thr	Asn	305	310	315	320
Ser	Gln	Val	Arg	Trp	Glu	Tyr	Cys	Lys	Ile	Pro	Ser	Cys	Asp	Ser	Ser	325	330	335	
Pro	Val	Ser	Thr	Glu	Gln	Leu	Ala	Pro	Thr	Ala	Pro	Pro	Glu	Leu	Thr	340	345	350	
Pro	Val	Val	Gln	Asp	Cys	Tyr	His	Gly	Asp	Gly	Gln	Ser	Tyr	Arg	Gly	355	360	365	
Thr	Ser	Ser	Thr	Thr	Thr	Thr	Gly	Lys	Lys	Cys	Gln	Ser	Trp	Ser	Ser	370	375	380	
Met	Thr	Pro	His	Arg	His	Gln	Lys	Thr	Pro	Glu	Asn	Tyr	Pro	Asn	Ala	385	390	395	400
Gly	Leu	Thr	Met	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Ala	Asp	Lys	Gly	Pro	405	410	415	
Trp	Cys	Phe	Thr	Thr	Asp	Pro	Ser	Val	Arg	Trp	Glu	Tyr	Cys	Asn	Leu	420	425	430	
Lys	Lys	Cys	Ser	Gly	Thr	Glu	Ala	Ser	Val	Val	Ala	Pro	Pro	Pro	Val	435	440	445	
Val	Leu	Leu	Pro	Asp	Val	Glu	Thr	Pro	Ser	Glu	Glu	Asp	Cys	Met	Phe	450	455	460	
Gly	Asn	Gly	Lys	Gly	Tyr	Arg	Gly	Lys	Arg	Ala	Thr	Thr	Val	Thr	Gly	465	470	475	480
Thr	Pro	Cys	Gln	Asp	Trp	Ala	Ala	Gln	Glu	Pro	His	Arg	His	Ser	Ile	485	490	495	
Phe	Thr	Pro	Glu	Thr	Asn	Pro	Arg	Ala	Gly	Leu	Glu	Lys	Asn	Tyr	Cys	500	505	510	

Arg Asn Pro Asp Gly Asp Val Gly Gly Pro Trp Cys Tyr Thr Thr Asn
 515 520 525
 Pro Arg Lys Leu Tyr Asp Tyr Cys Asp Val Pro Gln Cys Ala Ala Pro
 530 535 540
 Ser Phe Asp Cys Gly Lys Pro Gln Val Glu Pro Lys Lys Cys Pro Gly
 545 550 555 560
 Arg Val Val Gly Gly Cys Val Ala His Pro His Ser Trp Pro Trp Gln
 565 570 575
 Val Ser Leu Arg Thr Arg Phe Gly Met His Phe Cys Gly Gly Thr Leu
 580 585 590
 Ile Ser Pro Glu Trp Val Leu Thr Ala Ala His Cys Leu Glu Lys Ser
 595 600 605
 Pro Arg Pro Ser Ser Tyr Lys Val Ile Leu Gly Ala His Gln Glu Val
 610 615 620
 Asn Leu Glu Pro His Val Gln Glu Ile Glu Val Ser Arg Leu Phe Leu
 625 630 635 640
 Glu Pro Thr Arg Lys Asp Ile Ala Leu Leu Lys Leu Ser Ser Pro Ala
 645 650 655
 Val Ile Thr Asp Lys Val Ile Pro Ala Cys Leu Pro Ser Pro Asn Tyr
 660 665 670
 Val Val Ala Asp Arg Thr Glu Cys Phe Ile Thr Gly Trp Gly Glu Thr
 675 680 685
 Gln Gly Thr Phe Gly Ala Gly Leu Leu Lys Glu Ala Gln Leu Pro Val
 690 695 700
 Ile Glu Asn Lys Val Cys Asn Arg Tyr Glu Phe Leu Asn Gly Arg Val
 705 710 715 720
 Gln Ser Thr Glu Leu Cys Ala Gly His Leu Ala Gly Gly Thr Asp Ser
 725 730 735
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Phe Glu Lys Asp Lys
 740 745 750
 Tyr Ile Leu Gln Gly Val Thr Ser Trp Gly Leu Gly Cys Ala Arg Pro
 755 760 765
 Asn Lys Pro Gly Val Tyr Val Arg Val Ser Arg Phe Val Thr Trp Ile
 770 775 780
 Glu Gly Val Met Arg Asn Asn
 785 790

<210> 11

<211> 5

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Illustrative
RGD containing peptide

<400> 11
Gly Arg Gly Asp Ser
1 5

<210> 12
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Illustrative
RGD containing peptide

<400> 12
Gly Arg Gly Asp Thr Pro
1 5

<210> 13
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
6-His tag

<400> 13
His His His His His His
1 5

<210> 14
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Illustrative
peptide

<400> 14
Glu Lys Arg Glu Ala Glu Ala
1 5

<210> 15
<211> 4
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative
peptide

<400> 15

Leu Glu Lys Arg

1